

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/567,486  
Source: IFP  
Date Processed by STIC: 2/13/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 10/567,486

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length     The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4      Non-ASCII     The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5      Variable Length     Sequence(s)          contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)         . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7      Skipped Sequences  
    (OLD RULES)     Sequence(s)          missing. If intentional, please insert the following lines for **each** skipped sequence:  
                          (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                          (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          This sequence is intentionally skipped  
  
                          Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)     Sequence(s)          missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
                          <210> sequence id number  
                          <400> sequence id number  
                          000
- 9      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                          Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                          In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10     Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11     Use of <220>     Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
                          Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                          (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12     PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13     Misuse of n/Xaa     "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWP

## RAW SEQUENCE LISTING

DATE: 02/13/2006

PATENT APPLICATION: US/10/567,486

TIME: 12:41:39

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\02132006\J567486.raw

*see Item 2 on Even  
Summary Sheet*

3 <110> APPLICANT: CIPOLLONE, Francesco et al  
5 <120> TITLE OF INVENTION: Method and kit for assessing the risk of cardiovascular pathologies with

6 atheromatous etiology

8 <130> FILE REFERENCE: NOTAR9.001APC

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/567,486

C--> 10 <141> CURRENT FILING DATE: 2006-02-06

10 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/051711

11 <151> PRIOR FILING DATE: 2004-08-04

12 <150> PRIOR APPLICATION NUMBER: IT MI2003A001607

14 <151> PRIOR FILING DATE: 2003-08-05

16 <160> NUMBER OF SEQ ID NOS: 4

18 <170> SOFTWARE: PatentIn version 3.3

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 1400

22 <212> TYPE: DNA

23 <213> ORGANISM: Homo sapiens

26 <220> FEATURE:

27 <221> NAME/KEY: CDS

28 <222> LOCATION: (1335)..(1400)

29 <223> OTHER INFORMATION: Homo sapiens cyclooxygenase-2 (PTGS2) gene corresponding to  
30 Genbank accession number AF276953. Nucleotide in position 1371

31 can also be "t" or "g" or "c" Nucleotide polymorphism detected

32 on position 436, according to what?

35 <400> SEQUENCE: 1

36 ttccagctgt caaaatctcc cttccatcta attaattcct catccaacta tgttccaaaa 60  
38 cgagaataga aaattagccc caataagccc aggcaactga aaagtaaagt ctatgttgta 120  
40 ctttgatcca tggtcacaac tcataatctt ggaaaagtgg acagaaaaga caaaagagtg 180  
42 aactttaaaa ctcgaattta tttaccagt atctcctatg aagggttagt aacaaaata 240  
44 atccacgcat caggagagaga aatgccttaa ggcatacgtt ttggacattt agcgtccctg 300  
46 caaattctgg ccatcgccgc ttcctttgtc catcagaagg caggaaactt tatattggtg 360  
48 acccgtaggag ctcacattaa ctatttacag ggtaactgct taggaccagt attatgagga 420  
50 gaattttacct ttcccgcttc tctttccaag aaacaaggag ggggtgaagg tacggagaac 480  
52 agtattttctt ctgttgaaag caacttagct acaaagataa attacagcta tgtacactga 540  
54 aggtagctat ttcattccac aaaataagag ttttttaaaa agctatgtat gtatgtgctg 600  
56 catatagagc agatatacag cctattaagc gtcgtcacta aaacataaaa catgtcagcc 660  
58 tttcttaacc ttactcgccc cagtctgtcc cgacgtgact tcctcgaccc tctaaagacg 720  
60 tacagaccag acacggcggc ggcgccggga gaggggattc cctgcgcccc cggacctcag 780  
62 ggccgctcag attcctggag aggaagccaa gtgtccttct gccctcccc ggtatcccat 840  
64 ccaaggcagc cagtccagaa ctggctctcg gaagcgctcg ggcaagact gcgaagaaga 900  
66 aaagacactc ggcgggaaacc tgtgcgcctg gggcggtgga actcggggag gagaggagg 960  
68 gatcagacag gagagtgggg actacccctt ctgtcccaa attggggcag cttcctgggt 1020  
70 ttccgatttt ctcatctccg tgggtaaaaa accctgcccc caccgggctt acgcaatttt 1080  
72 ttttaagggga gaggagggaa aaatttgtgg ggggtacgaa aaggcggaaa gaaacagtca 1140

*pp 1-2*  
Does Not Comply  
Corrected Diskette Needed

*"a" (at  
location  
1371)*

*Can only  
represent  
itself. Use  
"n" instead,  
and  
explain in  
<2207-2223>  
section*

## RAW SEQUENCE LISTING

DATE: 02/13/2006

PATENT APPLICATION: US/10/567,486

TIME: 12:41:39

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\02132006\J567486.raw

```

74 tttcgtcaca tgggcttggt tttcagtcctt ataaaaagga aggttctctc ggtagcgac 1200
76 caattgtcat acgacttgca gtgagcgtca ggagcacgtc caggaactcc tcagcagcgc 1260
78 ctcccttcagc tccacagcca gacgccctca gacagcaaag cctacccccg cgccgcgccc 1320
80 tgccccgcgc tgcg atg ctc gcc cgc gcc ctg ctg ctg tgc gcg gtc ctg 1370
81 Met Leu Ala Arg Ala Leu Leu Leu Cys Ala Val Leu
82 1 5 10
84 acg ctc agc cat aca ggt gag tac ctg gcg 1400
85 Thr Leu Ser His Thr Gly Glu Tyr Leu Ala
86 15 20
89 <210> SEQ ID NO: 2
90 <211> LENGTH: 22
91 <212> TYPE: PRT
92 <213> ORGANISM: Homo sapiens
94 <400> SEQUENCE: 2
96 Met Leu Ala Arg Ala Leu Leu Leu Cys Ala Val Leu Thr Leu Ser His
97 1 5 10 15
100 Thr Gly Glu Tyr Leu Ala
101 20
104 <210> SEQ ID NO: 3
105 <211> LENGTH: 20
106 <212> TYPE: DNA
107 <213> ORGANISM: Homo sapiens
110 <220> FEATURE:
111 <221> NAME/KEY: primer_bind
112 <222> LOCATION: (1)..(20)
114 <400> SEQUENCE: 3
115 ccgcttcctt tgtccatcag 20
118 <210> SEQ ID NO: 4
119 <211> LENGTH: 21
120 <212> TYPE: DNA
121 <213> ORGANISM: Homo sapiens
124 <220> FEATURE:
125 <221> NAME/KEY: primer_bind
126 <222> LOCATION: (1)..(21)
128 <400> SEQUENCE: 4
129 gctatgtaca ctgaaggtag c 21

```

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/567,486

DATE: 02/13/2006  
TIME: 12:41:40

Input Set : A:\pto.da.txt  
Output Set: N:\CRF4\02132006\J567486.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

VERIFICATION SUMMARY

DATE: 02/13/2006

PATENT APPLICATION: US/10/567,486

TIME: 12:41:40

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\02132006\J567486.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date